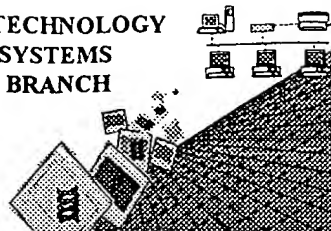BIOTECHNOLOGY
SYSTEMS
BRANCH

#19

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _09/634,287B_

Source: _1602_

Date Processed by STIC: _12/13/2002_

RECEIVED

DEC 2 0 2002

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
 PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
 PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER
VERSION 3.1 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission
   User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
   Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
           Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
   2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, r other delivery service to: U.S. Patent and Trademark Office,
   Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

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1600

RAW SEQUENCE LISTING   DATE: 12/13/2002
PATENT APPLICATION: **US/09/634,287B**   TIME: 14:49:42

Input Set : **A:\DM6909.ST25.txt**
Output Set: **N:\CRF4\12132002\I634287B.raw**

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 3 <110> APPLICANT: BRISTOL-MYERS SQUIBB COMPANY
 5 <120> TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
 7 <130> FILE REFERENCE: DM6090 DIV
 9 <140> CURRENT APPLICATION NUMBER: 09/634,287B
10 <141> CURRENT FILING DATE: 2000-08-09
12 <150> PRIOR APPLICATION NUMBER: 60/053,850
13 <151> PRIOR FILING DATE: 1997-07-25
15 <150> PRIOR APPLICATION NUMBER: 60/055,836
16 <151> PRIOR FILING DATE: 1997-08-15
18 <150> PRIOR APPLICATION NUMBER: 60/062,169
19 <151> PRIOR FILING DATE: 1997-10-16
21 <160> NUMBER OF SEQ ID NOS: 48
23 <170> SOFTWARE: PatentIn version 3.1
```

ERRORED SEQUENCES

Does Not Comply
Corrected Diskette Needed
pp 1-3

```
1243 <210> SEQ ID NO: 48
1244 <211> LENGTH: 16
1245 <212> TYPE: PRT
1246 <213> ORGANISM: dog
1248 <400> SEQUENCE: 48
1250 Thr Glu Pro Thr Val Ser Gln Glu Leu Ala Gln Arg Pro Pro Val Thr
1251 1             5              10             15
E--> 1257 (1
```

delete

see p. 2 for more error

```
371      770                  775              780
374 Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg Leu Arg Tyr Ser Phe
375 785                  790              795              800
378 Phe Val Pro Arg Pro Thr Pro Ser Thr Pro Arg Pro Thr Pro Gln Asp
379                  805              810              815
382 Trp Leu His Arg Arg Ala Gln Ile Leu Glu Ile Leu Arg Arg Arg Pro
383                  820              825              830
386 Trp Ala Gly Arg Lys
387          835
390 <210> SEQ ID NO: 3
391 <211> LENGTH: 0
392 <212> TYPE: DNA
393 <213> ORGANISM: Unknown
395 <220> FEATURE:
396 <223> OTHER INFORMATION: Blank Sequence
398 <400> SEQUENCE: 3
```
W--> **399 000**
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401 <210> SEQ ID NO: 4
402 <211> LENGTH: 26
403 <212> TYPE: PRT
404 <213> ORGANISM: Bos taurus
406 <400> SEQUENCE: 4
408 Phe Ala Ser Leu Ser Arg Val Glu Thr Leu Val Val Ala Asp Asp Lys
409 1              5              10              15
412 Met Ala Ala Phe His Gly Ala Gly Leu Lys
413              20              25
416 <210> SEQ ID NO: 5
417 <211> LENGTH: 7
418 <212> TYPE: PRT
419 <213> ORGANISM: Bos taurus
421 <400> SEQUENCE: 5
423 Tyr Thr Gly Val Ala Pro Arg
424 1              5
427 <210> SEQ ID NO: 6
428 <211> LENGTH: 11
429 <212> TYPE: PRT
430 <213> ORGANISM: Bos taurus
432 <400> SEQUENCE: 6
434 Ala Leu Gly Tyr Tyr Tyr Val Leu Asp Pro Arg
435 1              5              10
438 <210> SEQ ID NO: 7
439 <211> LENGTH: 21
440 <212> TYPE: DNA
441 <213> ORGANISM: Mus musculus
443 <400> SEQUENCE: 7
444 gggggtggtg tccagttctc c                                    21
447 <210> SEQ ID NO: 8
448 <211> LENGTH: 23
449 <212> TYPE: DNA
```

delete, Please use format shown in item 8 on Error Summary Sheet, for intentionally skipped sequences.

3

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\12182002\I634287B.raw**

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:21; Xaa Pos. 12

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _09/634,287B_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino
Numbering

The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001.